

=====

Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=9; day=8; hr=12; min=6; sec=15; ms=894; ]

=====

\*\*\*\*\*

Reviewer Comments:

<210> 1

<211> 776

<212> PRT

<213> mammalian

Although the above <213> response had been accepted in the previous 10/568396 submission, it is erroneous. The only valid <213> responses, per Sequence Rules, are: the Genus species of the organism, "Artificial Sequence", or "Unknown". "Artificial Sequence" and "Unknown" require explanation in the <220>-<223> section; please give the source of the genetic material. Same response in Sequence 2.

<210> 11

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

The above <223> response is an insufficient explanation of "Artificial Sequence": please clearly give the source of the genetic material. Same response in Sequences 12-14.

\*\*\*\*\*

Application No: 10568396 Version No: 2.0

**Input Set:**

**Output Set:**

**Started:** 2009-08-25 11:11:22.820  
**Finished:** 2009-08-25 11:11:24.257  
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 437 ms  
**Total Warnings:** 14  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 14  
**Actual SeqID Count:** 14

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)

SEQUENCE LISTING

<110> THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK

<120> ZAP PROTEIN AND RELATED COMPOSITIONS AND METHODS

<130> 67489-PCT/JPW/JW

<140> 10568396

<141> 2006-08-31

<150> PCT/US2004/026162

<151> 2004-08-12

<160> 14

<170> PatentIn version 3.5

<210> 1

<211> 776

<212> PRT

<213> mammalian

<400> 1

Met Ala Asp Pro Gly Val Cys Cys Phe Ile Thr Lys Ile Leu Cys Ala  
1 5 10 15

His Gly Gly Arg Met Thr Leu Glu Glu Leu Leu Gly Glu Ile Arg Leu  
20 25 30

Pro Glu Ala Gln Leu Tyr Glu Leu Leu Glu Thr Ala Gly Pro Asp Arg  
35 40 45

Phe Val Leu Leu Glu Thr Gly Gly Gln Ala Gly Ile Thr Arg Ser Val  
50 55 60

Val Ala Thr Thr Arg Ala Arg Val Cys Arg Arg Lys Tyr Cys Gln Arg  
65 70 75 80

Pro Cys Asp Ser Leu His Leu Cys Lys Leu Asn Leu Leu Gly Arg Cys  
85 90 95

His Tyr Ala Gln Ser Gln Arg Asn Leu Cys Lys Tyr Ser His Asp Val  
100 105 110

Leu Ser Glu Gln Asn Phe Gln Ile Leu Lys Asn His Glu Leu Ser Gly  
115 120 125

Leu Asn Gln Glu Glu Leu Ala Cys Leu Leu Val Gln Ser Asp Pro Phe  
130 135 140

Phe Leu Pro Glu Ile Cys Lys Ser Tyr Lys Gly Glu Gly Arg Lys Gln  
145 150 155 160

Thr Cys Gly Gln Pro Gln Pro Cys Glu Arg Leu His Ile Cys Glu His  
165 170 175

Phe Thr Arg Gly Asn Cys Ser Tyr Leu Asn Cys Leu Arg Ser His Asn  
180 185 190

Leu Met Asp Arg Lys Val Leu Thr Ile Met Arg Glu His Gly Leu Ser  
195 200 205

Pro Asp Val Val Gln Asn Ile Gln Asp Ile Cys Asn Asn Lys His Ala  
210 215 220

Arg Arg Asn Pro Pro Gly Thr Arg Ala Ala His Pro His Arg Arg Gly  
225 230 235 240

Gly Ala His Arg Asp Arg Ser Lys Ser Arg Asp Arg Phe Leu His Asn  
245 250 255

Ser Leu Glu Phe Leu Ser Pro Val Val Ser Pro Leu Gly Ser Gly Pro  
260 265 270

Pro Ser Pro Asp Val Thr Ser Cys Lys Asp Ser Leu Glu Asp Val Ser  
275 280 285

Val Asp Val Thr Gln Lys Phe Lys Tyr Leu Gly Thr His Asp Arg Ala  
290 295 300

Gln Leu Ser Pro Val Ser Ser Lys Ala Ala Gly Val Gln Gly Pro Ser  
305 310 315 320

Gln Met Arg Ala Ser Gln Glu Phe Ser Glu Asp Gly Asn Leu Asp Asp  
325 330 335

Ile Phe Ser Arg Asn Arg Ser Asp Ser Ser Ser Arg Ala Ser Ala  
340 345 350

Ala Lys Val Ala Gln Arg Asn Glu Ala Val Ala Met Lys Met Gly Met

355

360

365

Glu Val Lys Gly Lys Lys Glu Ala Pro Asp Ile Asp Arg Val Pro Phe  
370 375 380

Leu Asn Ser Tyr Ile Asp Gly Val Thr Met Glu Lys Ala Ser Val Ser  
385 390 395 400

Gly Ile Pro Gly Lys Lys Phe Thr Ala Asn Asp Leu Glu Asn Leu Leu  
405 410 415

Leu Leu Asn Asp Thr Trp Lys Asn Val Ala Lys Pro Gln Asp Leu Gln  
420 425 430

Thr Thr Gly Arg Ile Thr Asp Ser Gly Gln Asp Lys Ala Phe Leu Gln  
435 440 445

Asn Lys Tyr Gly Gly Asn Pro Val Trp Ala Ser Ala Ser Thr His Asn  
450 455 460

Ala Pro Asn Gly Ser Ser Gln Ile Met Asp Glu Thr Pro Asn Val Ser  
465 470 475 480

Lys Ser Ser Thr Ser Gly Phe Ala Ile Lys Pro Ala Ile Ala Gly Gly  
485 490 495

Lys Glu Ala Val Tyr Ser Gly Val Gln Ser Pro Arg Ser Gln Val Leu  
500 505 510

Ala Val Pro Gly Glu Ala Thr Thr Pro Val Gln Ser Asn Arg Leu Pro  
515 520 525

Gln Ser Pro Leu Ser Ser Ser His Arg Ala Ala Ala Ser Gly Ser  
530 535 540

Pro Gly Lys Asn Ser Thr His Thr Ser Val Ser Pro Ala Ile Glu Ser  
545 550 555 560

Ser Arg Met Thr Ser Asp Pro Asp Glu Tyr Leu Leu Arg Tyr Ile Leu  
565 570 575

Asn Pro Leu Phe Arg Met Asp Asn His Gly Pro Lys Glu Ile Cys Gln  
580 585 590

Asp His Leu Tyr Lys Gly Cys Gln Gln Ser His Cys Asp Arg Ser His  
595 600 605

Phe His Leu Pro Tyr Arg Trp Gln Met Phe Val Tyr Thr Thr Trp Arg  
610 615 620

Asp Phe Gln Asp Met Glu Ser Ile Glu Gln Ala Tyr Cys Asp Pro His  
625 630 635 640

Val Glu Leu Ile Leu Ile Glu Asn His Gln Ile Asn Phe Gln Lys Met  
645 650 655

Thr Cys Asp Ser Tyr Pro Ile Arg Arg Leu Ser Thr Pro Ser Tyr Glu  
660 665 670

Glu Lys Pro Leu Ser Ala Val Phe Ala Thr Lys Trp Ile Trp Tyr Trp  
675 680 685

Lys Asn Glu Phe Asn Glu Tyr Ile Gln Tyr Gly Asn Glu Ser Pro Gly  
690 695 700

His Thr Ser Ser Asp Ile Asn Ser Ala Tyr Leu Glu Ser Phe Phe Gln  
705 710 715 720

Ser Cys Pro Arg Gly Val Leu Pro Phe Gln Ala Gly Ser Gln Lys Tyr  
725 730 735

Glu Leu Ser Phe Gln Gly Met Ile Gln Thr Asn Ile Ala Ser Lys Thr  
740 745 750

Gln Arg His Val Val Arg Arg Pro Val Phe Val Ser Ser Asn Asp Val  
755 760 765

Glu Gln Lys Arg Arg Gly Pro Glu  
770 775

<210> 2  
<211> 2331  
<212> DNA  
<213> mammalian

<400> 2  
atggcagatc ccggggatcg ctgtttcatc accaagatcc tgcgcgccca cggggggccgt 60

atgaccctgg aggaactgct gggtagagatc aggctccccg aggccgcagct ctacgagctg 120  
ctggagacgg cggggcccgta tcgttcgtt ctattggaga ctggaggcca ggccgggatc 180  
actcggtctg tagtggtcac tactcgagcc cgctgtcgcc gtccggaaatc ctgccagaga 240  
ccctgcgaca gcctgcacct ctgcaagctt aatctgtcg gccgggtgcca ctatgcacag 300  
tctcagcggaa acctctgcaa atattctcac gatgttctct cggAACAGAA cttccagatc 360  
ctgaagaatc atgagcttc tgggcttaac caagaggagc tagcttgccc cctggtccaa 420  
agcgaccctt ttttctgcc cgagatatgc aagagtata aaggagaggg ccgaaaacag 480  
acctgtggc agccacagcc atgcgagaga ctccacatct gtgagcactt cacccggggc 540  
aactgcagtt acctaactg tctcaggatct cacaacctga tggacagaaa ggtgttgacc 600  
atcatgaggg agcacgggct gagtcctgtat gtggccaga acatccagga catctgcaac 660  
aacaaacacg ccaggaggaa cccgcctggc acgagagctg cccatccaca ccgcagaggc 720  
ggcgcacaca gagacagaag caaaagcaga gaccgcttcc ttccacaacag tctagaattt 780  
ctctcacctg ttgtctcacc tctggatct ggtccgccta gcccagatgt caccagctgt 840  
aaagattccc tggaggatgt gtctgtggat gtcaccaga agttcaagta ctggggacg 900  
catgaccgtg cgccagcttc cccagtcata tctaaggctg ctggtgttca aggacccagt 960  
caaatgagag caagccaaga gtttcagag gatggaaatc tagatgacat atttctagg 1020  
aatcgttctg attcatcatc aagtgcgagcc tccgctgccaa aggtggcaca aagaaatgaa 1080  
gctgtggcca tgaaaatggg catggaggta aaggcaaga aggaggctcc agacatcgat 1140  
cgggtcccat tttaaatag ttatattgt ggggtgacca tggaaaaagc atcggtctca 1200  
ggaattccag gcaaaaagtt cacagccaaat gatctggaaa atttgctatt acttaacgac 1260  
acttggaaatgtggctaa gccccaggat ctgcagacca caggcagaat cactgacagt 1320  
ggccaagaca aggcattcct gcagaataaa tatggaggaa acccagtgtg ggcaagtgc 1380  
tccacccata atgccccaaa tggctctagt caaattatgg atgaaactcc taatgtct 1440  
aaaagtagta ccagtggtt tgccataaaa ccagcaattt gttggggaaa agaaggcgtc 1500  
tattctggag ttctcagatcc gagaagccag gtccttagctg tgcctggggaa ggctactacc 1560  
cctgtacaga gcaacaggct gcctcagtcg cctctgtttt cctcaagccaa cagagctgca 1620  
gcctctggaa gcccggccaa gaactccacc catacctctg tggcccgacg catcgatct 1680  
tcaaggatga catcagaccc cgtatgtatc ttcctacgct acatcctaaa tcctttatct 1740

aggatggata atcatggccc gaaggaaatc tgtcaggacc atctgtacaa gggctgtcaa	1800
cagagccact gcgacaggag tcacttccat ctgccttacc ggtggcagat gttcgatat	1860
accacttgg a gggacttcca ggacatggag tctatcgaac aggcttattg tgatccccac	1920
gttgaactca ttttgataga aaaccatcag atcaattcc agaaaatgac ctgtgactcc	1980
taccccatcc gacgcctctc cactccctca tatgaggaaa agccacttag tgctgtctc	2040
gccaccaagt ggatttggta ttggaagaat gaatttaatg aatatatcca gtatggaat	2100
gagagcccaag gccacaccag ctctgacatc aactctgcgt acctggagtc tttcttccag	2160
tcttgtccca ggggagttt gccattccag gctggttcac agaagtacga gttaagcttc	2220
caagggatga ttccagacaaa tatacgcc aagactcaaa ggcatgttgt cagaaggcca	2280
gtatgtttt cttcgAACGA tttggagcag aagagaagag gtccagagt a	2331

<210> 3  
<211> 78  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR Primer

<400> 3  
ataagcttgc caccatggct tttccststg stgttcaga tatgtctaat tcggcgccg 60  
cgccaaagttg accagtgc 78

<210> 4  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR Primer

<400> 4  
atatcgattc agtcctgctc ctccgc 26

<210> 5  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 5  
ctagataact tcgtataatg tatgtataac gaagttat 38

<210> 6  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 6  
ctagataact tcgtatagca tacattatac gaagttat 38

<210> 7  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR Primer

<400> 7  
gcttatccat atgatgttcc agatt 25

<210> 8  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR Primer

<400> 8  
atataaggcgg ccgcaccttg gacctttct cttc 34

<210> 9  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR Primer

<400> 9  
gagctctctg ggcttaacc 19

<210> 10  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR Primer

<400> 10  
atataaggcgg ccgcctctg gacctttct cttc

34

<210> 11  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> peptide

<400> 11

Cys Arg Arg Lys Tyr Cys Gln Arg Pro Cys Asp Ser Leu His  
1 5 10

<210> 12  
<211> 23  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> peptide

<400> 12

Cys Lys Leu Asn Leu Leu Gly Arg Cys His Tyr Ala Gln Ser Gln Arg  
1 5 10 15

Asn Leu Cys Lys Tyr Ser His  
20

<210> 13  
<211> 23  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> peptide

<400> 13

Cys Lys Ser Tyr Lys Gly Glu Gly Arg Lys Gln Thr Cys Gly Gln Pro  
1 5 10 15

Gln Pro Cys Glu Arg Leu His  
20

<210> 14  
<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 14

Cys Glu His Phe Thr Arg Gly Asn Cys Ser Tyr Leu Asn Cys Leu Arg

1 5 10

15

Ser His